RAW SEQUENCE LISTING   DATE: 11/28/2001
PATENT APPLICATION: US/09/910,186A   TIME: 13:08:12

Input Set : A:\09910186seqlist.txt
Output Set: N:\CRF3\11212001\I910186A.raw   **ENTERED**

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        1 <110> APPLICANT: U.S. Army Medical Research & Material Command
        4 <120> TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
        5       NEUROTOXIN
        7 <130> FILE REFERENCE: A33626-A 067252.0107
C-->    9 <140> CURRENT APPLICATION NUMBER: US/09/910,186A
C-->    9 <141> CURRENT FILING DATE: 2001-07-20
        9 <150> PRIOR APPLICATION NUMBER: PCT/US00/12890
       10 <151> PRIOR FILING DATE: 2000-05-12
       12 <150> PRIOR APPLICATION NUMBER: 09/611,419
       13 <151> PRIOR FILING DATE: 2000-07-06
       15 <150> PRIOR APPLICATION NUMBER: 60/133,865
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       18 <150> PRIOR APPLICATION NUMBER: 60/133,866
       19 <151> PRIOR FILING DATE: 1999-05-12
       21 <150> PRIOR APPLICATION NUMBER: 60/133,867
       22 <151> PRIOR FILING DATE: 1999-05-12
       24 <150> PRIOR APPLICATION NUMBER: 60/133,868
       25 <151> PRIOR FILING DATE: 1999-05-12
       27 <150> PRIOR APPLICATION NUMBER: 60/133,869
       28 <151> PRIOR FILING DATE: 1999-05-12
       30 <150> PRIOR APPLICATION NUMBER: 60/133,873
       31 <151> PRIOR FILING DATE: 1999-05-12
       33 <150> PRIOR APPLICATION NUMBER: 08/123,975
       34 <151> PRIOR FILING DATE: 1993-09-21
       36 <160> NUMBER OF SEQ ID NOS: 34
       38 <170> SOFTWARE: FastSEQ for Windows Version 4.0
       40 <210> SEQ ID NO: 1
       41 <211> LENGTH: 1332
       42 <212> TYPE: DNA
       43 <213> ORGANISM: Artificial Sequence
       45 <220> FEATURE:
       46 <223> OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
       47       sequence
       49 <221> NAME/KEY: CDS
       50 <222> LOCATION: (13)...(1326)
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       55             Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
       56              1               5                      10
       58 atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg   99
       59 Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
       60      15              20                  25
       62 atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt   147
       63 Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
       64   30              35                  40                  45
       66 aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa   195
       67 Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
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68                  50                  55                  60
70 tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct    243
71 Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
72                  65                  70                  75
74 atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac    291
75 Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
76          80                  85                  90
78 ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg    339
79 Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
80      95                  100                 105
82 gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc    387
83 Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
84 110                 115                 120                 125
86 tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa    435
87 Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
88                  130                 135                 140
90 tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc    483
91 Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
92          145                 150                 155
94 gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac    531
95 Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
96          160                 165                 170
98 ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac    579
99 Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
100     175                 180                 185
102 gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac   627
103 Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
104 190                 195                 200                 205
106 cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac   675
107 Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
108                 210                 215                 220
110 gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc   723
111 Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
112                 225                 230                 235
114 ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac   771
115 Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr
116         240                 245                 250
118 atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta   819
119 Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
120     255                 260                 265
122 ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg   867
123 Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
124 270                 275                 280                 285
126 act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc   915
127 Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
128                 290                 295                 300
130 atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac   963
131 Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
132                 305                 310                 315
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134 aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt   1011
135 Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
136         320             325             330
138 ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct   1059
139 Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
140         335             340             345
142 ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa   1107
143 Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
144 350             355             360             365
146 tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag   1155
147 Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
148         370             375             380
150 gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac   1203
151 Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
152         385             390             395
154 aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa   1251
155 Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
156         400             405             410
158 cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat   1299
159 Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
160         415             420             425
162 gac ggt tgg ggt gaa cgt ccg ctg taa gaattc                        1332
163 Asp Gly Trp Gly Glu Arg Pro Leu  *
164 430             435
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 437
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
174        sequence
177 <400> SEQUENCE: 2
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179 1           5               10              15
180 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
181         20              25              30
182 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
183         35              40              45
184 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
185     50              55              60
186 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
187 65              70              75              80
188 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
189             85              90              95
190 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
191         100             105             110
192 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
193         115             120             125
194 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
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Output Set: N:\CRF3\11212001\I910186A.raw

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195      130                    135                    140
196 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
197 145                    150                    155                    160
198 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
199                    165                    170                    175
200 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
201                    180                    185                    190
202 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
203             195                    200                    205
204 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
205      210                    215                    220
206 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
207 225                    230                    235                    240
208 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
209                    245                    250                    255
210 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
211                    260                    265                    270
212 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
213             275                    280                    285
214 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
215      290                    295                    300
216 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
217 305                    310                    315                    320
218 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
219                    325                    330                    335
220 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
221             340                    345                    350
222 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
223             355                    360                    365
224 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
225      370                    375                    380
226 Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
227 385                    390                    395                    400
228 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
229             405                    410                    415
230 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
231             420                    425                    430
232 Gly Glu Arg Pro Leu
233             435
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 1323
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Synthetic construct based on Clostridium botulinum
243       sequence
246 <221> NAME/KEY: CDS
247 <222> LOCATION: (13)...(1314)
248 <223> OTHER INFORMATION: Synthetic Construct
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PATENT APPLICATION: US/09/910,186A   TIME: 13:08:12

Input Set : A:\09910186seqlist.txt
Output Set: N:\CRF3\11212001\I910186A.raw

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253                1               5                  10
255 acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg    99
256 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
257      15                  20                  25
259 tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat   147
260 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
261   30                  35                  40                  45
263 ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa   195
264 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
265               50                  55                  60
267 atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa   243
268 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
269               65                  70                  75
271 aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc   291
272 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
273           80                  85                  90
275 atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat   339
276 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
277       95                  100                 105
279 tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg   387
280 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
281 110                 115                 120                 125
283 cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag   435
284 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
285               130                 135                 140
287 atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc   483
288 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
289               145                 150                 155
291 acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg   531
292 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
293           160                 165                 170
295 atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat   579
296 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
297       175                 180                 185
299 aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc   627
300 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
301 190                 195                 200                 205
303 tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa   675
304 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
305               210                 215                 220
307 atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac   723
308 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
309               225                 230                 235
311 ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat   771
312 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
313           240                 245                 250
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VERIFICATION SUMMARY   DATE: 11/28/2001
PATENT APPLICATION: **US/09/910,186A**   TIME: 13:08:13

Input Set : **A:\09910186seqlist.txt**
Output Set: **N:\CRF3\11212001\I910186A.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date